

	340		360		380		400	
Pg_3CAR1	-----	-----	-----	-----	-----	CGATAACGTT	GAACGATTGG	GGATCGACAG 30
Pg_3CAR2	-----	-----	-----	-----	-----	CGATAACGTT	GAACGATTGG	GGATCGACAG 30
Pg_3CAR3	-----	-----	-----	-----	-----	CGATAACGTT	GAACGATTGG	GGATCGACAG 30
Pg_3CAR4	-----	-----	-----	-----	-----	CGATAACGTT	GAACGATTGG	GGATCGACAG 30
Ps_Q09	GGAGAAITTAG	TGAGTCATGT	CGATGATCTC	CTTCAACACC	TTTCGATGGT	CGATAACGTT	GAACGATTGG	GGATCGACAG 80
	420		440		460		480	
Pg_3CAR1	ACATTTCCAA	ACTGAGATCA	AAGTTTCCCT	CGATTATGTT	TACAGGTCAG	TGCTGACAGC	CTTCAAATTT	TTTTATGTT 110
Pg_3CAR2	ACATTTCCAA	GCTGAGATAA	AAGTTTCCCT	CGATTATGTT	TACAGGTCAG	TGCTGACAGC	CTTCAAATTT	TTTTATGTT 110
Pg_3CAR3	ACATTTCCAA	ACTGAGATAA	AAGTTTCCCT	CGATTATGTT	TACAGGTCAG	TGCTGACAGC	CTTCAAATTT	TTTTATGTT 110
Pg_3CAR4	ACATTTCCAA	ACTGAGATAA	AAGTTTCTCT	TGATTATGTT	TACAGGTCAG	TGCTGACGGC	CTTCAAATTT	TTGTTATGTT 110
Ps_Q09	ACATTTCCAA	ACTGAGATCA	AAGTTTCCCT	CGATTATGTT	TACAG-----	-----	-----	----- 125
	500		520		540		560	
Pg_3CAR1	TTCACGACGA	ATACACTTAA	AACATAGAAA	TTATTTTGGC	CACCAGTT - A	CTGGAGCGAA	AAAGGCATTG	GACCTGGGAG 189
Pg_3CAR2	TTCACGACGA	ATACACTTAA	AACATAGAAA	TTATTTTGGC	CACCAGTT - A	CTGGAGCGAA	AAAGGCATTG	GACCTGGGAG 189
Pg_3CAR3	TTCACGACGA	ATACACTTAA	AACATAGAAA	TTATTTTGGC	CACCAGTT - A	CTGGAGCGAA	AAAGGCATTG	GACCTGGGAG 190
Pg_3CAR4	TTCACGACGA	ATACACTTAA	AACATAGAAA	TTATTTTGGC	CACCAGTT - A	CTGGAGCGAA	AAAGGCATTG	GATCTGGGAG 189
Ps_Q09	-----	-----	-----	-----	TT - A	CTGGAGCGAA	AAAGGCATTG	GACCTGGGAG 158
	580		600		620		640	
Pg_3CAR1	AGATATTGTT	TGTGCTGATC	TCAACACCAC	TGCCTTGGGG	TTTCGAGTTC	TTCGACTACA	TGGATATACT	GTGTTTCCAG 269
Pg_3CAR2	AGATATTGTT	TGTGCTGATC	TCAACACCAC	TGCCTTGGGG	TTTCGACTTC	TTCGACTACA	TGGATATACT	GTGTTTCCAG 269
Pg_3CAR3	AGATATTGTT	TGTGCTGATC	TCAACACGAC	TGCCTTGGGG	TTTCGAGTTC	TTCGACTACA	TGGATATACT	GTGTTTCCGG 270
Pg_3CAR4	AGATATTGTT	TGTACTGATC	TGAACACAAC	TGCCTTGGGG	TTTCGAAATC	TTCGACTACA	TGGATATACT	GTGTTCCGG 269
Ps_Q09	AGATATTGTT	TGTGCTGATC	TCAACACCAC	TGCCTTGGGG	TTTCGACTTC	TTCGACTACA	TGGATATACT	GTGTTTCCAG 238
	660		680		700		720	
Pg_3CAR1	GTATCCGCAT	TTTATTGATA	AATCCCTCCT	TTATTTTCTT	TAATAAGGCA	AC-----	-----	----- 321
Pg_3CAR2	GTATCCGCAT	TTTATTGATA	AATCCCTCCT	TTATTTTCTT	TAATAAGGCA	TCTGCGTGTA	GATATTGATA	GTTATATGTA 349
Pg_3CAR3	GTATCCACAT	TTTATTGATA	AATCACTCCT	TTATTTTCTT	TAATAAGGCA	TC-----	-----	----- 322
Pg_3CAR4	GTATCCACAT	TTTATTGATA	AATCACTCCT	TTATTTTCTT	TAATAAGGCA	TC-----	-----	----- 321
Ps_Q09	-----	-----	-----	-----	-----	-----	-----	----- 238
	740		760		780		800	
Pg_3CAR1	-----	-----	TGCGTGTAGA	TATTGATAGT	TATATGTATT	TTACGTTTAT	GTCAGACGTG	TTTGAACAAT 381
Pg_3CAR2	TTTACGTTT	ATGTCAGACG	TGCGTGTAGA	TATTGATAGT	TATATGTATT	TTACGTTTAT	GTCAGACGTG	TTTGAACAAT 429
Pg_3CAR3	-----	-----	TGCGTGTAGA	TATTGATAGT	TATATGTATT	TTACGTTTAT	GTCAGACGTG	TTTGAACAAT 382
Pg_3CAR4	-----	-----	TGCGTGTAGA	TATTGATAGT	TATATGTATT	TTACGTTTAT	GTCAGACGTG	TTTGAACAAT 381
Ps_Q09	-----	-----	-----	-----	-----	-----	-----ACGTG	TTTGAACAAT 253
	820		840		860			
Pg_3CAR1	TCAAAGACCA	GATGGGGCGG	ATTGCCTGTT	CCACCAATCA	GACAGAG	428		
Pg_3CAR2	TCAAAGACCA	GATGGGGCGG	ATTGCCTGTT	CCACCAATCA	GACAGAG	476		
Pg_3CAR3	TCAAAGACCA	GATGGGGCGG	ATTGCCTGTT	CCACCAATCA	GACAGAG	429		
Pg_3CAR4	TCAAAGACCA	GATGGGGCGG	ATTGCCTGTT	CCACCAATCA	GACAGAG	428		
Ps_Q09	TCAAAGACCA	GATGGGGCGG	ATTGCCTGTT	CCACCAATCA	GACAGAG	300		